IN THE SPECIFICATION

Replace Table 2 on page 11 with Table 2 submitted herewith, indicating SEQ ID NOS. of the illustrated sequences.

Replace the paragraph beginning "Table 3 shows" on page 12 of the specification with the following paragraph.

Table 3 shows alignment of cDNA sequences from the polyprotein coding sequences of the Ljungan 145SL isolate [SEQ ID NO. 4] to the amino acid sequences of sequenced cardioviruses in the comparative alignment compiled by Dr. A. Palmenberg (personal comm.). Table 3 show the alignment of Ljungan 145 SL [SEQ ID NO. 4], TMEBeAn [SEQ ID NO. 8], TMEGd7 [SEQ ID NO. 9], TMEGd7b [SEQ ID NO. 10], TMEDa [SEQ ID NO. 11], Vilyuisk [SEQ ID NO. 12], EMCBd [SEQ ID NO. 13], EMCBc [SEQ ID NO. 14], EMCDd [SEQ ID NO. 15], EMCDc [SEQ ID NO. 16], EMCDv1 [SEQ ID NO. 17], EMCR [SEQ ID NO. 18], MengoM [SEQ ID NO. 19] and Mengo37a [SEQ ID NO. 20]. The TMEBeAn strain was arbitrarily taken as the indicator strain, while the amino acids of the remaining strains are shown only if they differ from the indicator strain. For the Ljungan 145SL isolate, similar, but non-identical amino acids are indicated in small type. The amino acid homology between Ljungan 145SL and other cardioviruses was established screening the entire Swiss Protein Data Bank using the BLITZ search algorithm with standard search parameters.

2

TABLE 2

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1. AGTCTAGTCTTATCTTGTATGTGTCCTGCACT..GA..ACTTGTTTCTGT
2. AGTCTAGTTTCATTCTGTGTGTGTTTGGCACT..GA..AATTATTTCTGT
3. AGTTTGGTTCTCTCTTGAGTGTGTTTTGTGTT..AG..CATAATTTCTGT
4. TGACAGG.GTTATTTTCACC.TCTTCTT..TTCTACTCCACAG.TG.T.T
5. TGACAGG.GTTATTTTCACC.TCTTCTCTCTTCTACTTCATAG.TG.T.T
6. AGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCAC..CATA.TTGCCGT
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1. CTCTGGAGTGCTCTACACTTCAGTAGGGGCTGT.A.CCCGGGCGGTCCCA
2. CTCTGGGGTGCTTTACACTTCAGTAGGGGCTGT.A.CCCGGGCGGTCCCA
3. CTCTAGAGTGCTTTACACTCTAGTAGGGGCTGT.A.CCCGGGCGGTCCCA
4. CT.A.........TACTGTG..GAAGGGTATGTGT....TGCCCCTTCCT
5. CT.A.........TACTATG.AA.AGGGTATGTGT..C..GCCCCTTCCT
6. CT.T.......TTGGCAATGT.G.AGGGCCCG.GAAACCTGGCCCTGTCT
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1. CTCTTCACAGGAATCTGCACAGGTGGCTTTCAC.CTCTGGACAGTGCATT
2. CTCTTCACAGGAATNTGCACAGGTGGCTTTCAC.CTCTGGACAGTGCATT
3. CTCTTCACAGGAATCTGCACAGGTGGCTTTCAC.CTCTGGACAGTGCATT
4. .TCTTGGAGAACGT..GCGCGGCGGTCTTTCCGTCTCTCGACAA.GCGC.
5. .TCTTGGAGAACGT..GCGTGGCGGTCTTTCCGTCTCTCGAAAAACG..T
6. .TCTTGACGAGCAT.T.CCTAGGGGTCTTTCCC.CTCTCGCCAAAGGAAT
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1. CCACACCCG.C.TCCACGGTAGAAGATGATGTGTGTCTTTGCT..TGTGA
2. CCACACCCG.C.TCCACAGTAGAAGATGATGTGTGTCTTTGCT..TGTGA
3. CCATACCCG.C.TCCACAATAGAAGATGATGTATATCTTTGTT..TGTGA
4. GCGT..GCAACATACAGAGT.AACG.CGAAGAA.AGCA..GTTC.TC.GG
5. GCGT..GCGACATGCAGAGT.AACG.CAAAGAA.AGCA..GTTC.T.TGG
6. GCA.A.G.GTC.TGTTGAAT.GTCG.TGAAGGA.AGCA..GTTCCTCTGG
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1. AAA.GCTT...GTGAAAATC.........GTGTGTAGGCGTAGCGGCTACT
2. AAA.GCTT...GTGAAAATC.........GTGTGTAGGCGTAGCGGNTACT
3. AAT.GCT.CA..TGAA.A.C......GTGTGTGTAGGCGTAGCGGCTACT
4. TCTAGCT.CTAGTGCCCA.CAAGAAAACAGCTGTAG.CG.ACCA.C.ACA
5. TCTAGCT.CTGGTGCCCA.CAAGAAAACAGCTGTAG.CG.ACCA.C.ACA
6. AA..GCTTCT..TGAAGA.CAA.ACAACGTCTGTAG.CG.ACC..CT..T
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1. TGAGTGCCAGCGGATTACCCCTAGTGGTAACACTAGC    [SEQ ID NO: 1]
2. TGAGTGCCAGCGGACNACCCCTAGTGGTAACACTAGC    [SEQ ID NO: 2]
3. TGAATGCCAGCGGAACCCCCCTAGTGGTAACACTAGC    [SEQ ID NO: 3]
4. ..AAGGC.AGCGGAACCCCCCTCCTGGTAACAGGAGC    [SEQ ID NO: 5]
5. ..AAGGC.AGCGGAAACCCCCTCCTGGTAACAGGAGC    [SEQ ID NO: 6]
6. TGCAGGC.AGCGGAACCCCCCACCTGGCGACAGGTGC    [SEQ ID NO: 7]
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In this region of the viral genome, Ljungan 174F has 94% homology to Ljungan 87-012 (here taken as the indicator strain for comparisons), and Ljungan 145SL